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TEAM 8

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/896,589*

DATE: 09/03/97
TIME: 13:27:20

INPUT SET: S20087.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Burnham, Martin K.

(ii) TITLE OF THE INVENTION: NOVEL XANTHINE PHOSPHORIBOSYL TRANSFERASE

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Dechert Price & Rhoads
(B) STREET: 997 Lenox Drive, Building 3, Suite 210
(C) CITY: Lawrenceville
(D) STATE: NJ
(E) COUNTRY: USA
(F) ZIP: 08543

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Bloom, Allen
(B) REGISTRATION NUMBER: 29,135
(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 609-520-3214
(B) TELEFAX: 609-520-3259
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATGAAATTAT TAGAAGAGCG CATCCTCAAG GATGGGCATA TCTTGGGTGA TAACATCCTC     60
AAGGTAGATT CCTTTTTAAC CCACCAAGTT GACTTTAGCT TGATGCGAGA GATTGGTAAG    120
GTTTTTGCGG AAAAATTTGC TGCTACTGGC ATTACCAAGG TCGTAACCAT TGAAGCGTCG    180
GGTATTGCCC CAGCCGTTTT TACAGCTGAA GCCTTAAACG TTCCCATGAT TTTCGCCAAA    240
AAAGCTAAGA ACATCACCAT GAACGAAGGC ATCTTAACTG CTCAAGTCTA CTCCTTTACC    300
AAGCAGGTGA CCAGCACTGT TTCTATCGCT GGAAAATTCC TCTCACCAGA GGACAAGGTT    360
TTGATTATCG ACGATTTCCT TGCTAATGGC CAAGCTGCTA AAGGCTTGAT TCAAATCATC    420
GAACAGGCCG GTGCCACAGT CCAAGCTATC GGTATCGTGA TTGAGAAATC CTTCCAAGAT    480
GGTCGTGATT TGCTTGAAAA AGCAGGCTAC CCTGTCCTAT CACTTGCTCG CTTGGATCGT    540
TTTGAAAATG GTCAGGTCGT ATTTAAGGAG GCAGATCTCT AA                       582
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Lys Leu Leu Glu Glu Arg Ile Leu Lys Asp Gly His Ile Leu Gly
 1               5                  10                  15
Asp Asn Ile Leu Lys Val Asp Ser Phe Leu Thr His Gln Val Asp Phe
            20                  25                  30
Ser Leu Met Arg Glu Ile Gly Lys Val Phe Ala Glu Lys Phe Ala Ala
        35                  40                  45
Thr Gly Ile Thr Lys Val Val Thr Ile Glu Ala Ser Gly Ile Ala Pro
    50                  55                  60
Ala Val Phe Thr Ala Glu Ala Leu Asn Val Pro Met Ile Phe Ala Lys
65                  70                  75                  80
Lys Ala Lys Asn Ile Thr Met Asn Glu Gly Ile Leu Thr Ala Gln Val
                85                  90                  95
Tyr Ser Phe Thr Lys Gln Val Thr Ser Thr Val Ser Ile Ala Gly Lys
            100                 105                 110
Phe Leu Ser Pro Glu Asp Lys Val Leu Ile Ile Asp Asp Phe Leu Ala
        115                 120                 125
Asn Gly Gln Ala Ala Lys Gly Leu Ile Gln Ile Ile Glu Gln Ala Gly
    130                 135                 140
Ala Thr Val Gln Ala Ile Gly Ile Val Ile Glu Lys Ser Phe Gln Asp
```

```
145                 150                 155                 160
Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala
                165                 170                 175
Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp
            180                 185                 190
Leu
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
ATGAAATTAT TAGAAGAGCG CATCCTCAAG GATGGGCATA TCTTGGGTGA TAACATCCTC     60
AAGGTAGATT CCTTTTTAAC CCACCAAGTT GACTTTAGCT TGATGCGAGA GATTGGTAAG    120
GTTTTTGCGG AAAAATTTGC TGCTACTGGC ATTACCAAGG TCGTAACCAT TGAAGCGTCG    180
GGTATTGCCC CAGCCGTTTT TACAGCTGAA GCCTTAAACG TTCCCATGAT TTTCGCCAAA    240
AAAGCTAAGA ACATCACCAT GAACGAAGGC ATCTTAACTG CTCAAGTCTA CTCCTTTACC    300
AAGCAGGTGA CCAGCACTGT TTCTATCGCT GGAAAATTCC TCTCACCAGA GGACAAGGTT    360
TTGATTATCG ACGATTTCCT TGCTAATGGC CAAGCTGCTA AAGGCTTGAT TCAAATCATC    420
GAACAGGCCG GTGCCACAGT CCAAGCTATC GGTATCGTGA TTGAGAAATC CTTCCAAGAT    480
GGTCGTGATT TGCTTGAAAA AGCAGGCTAC CCTGTCCTAT CACTTGCTCG CTTGGATCGT    540
TTTGAAAATG GTCAGGTCGT ATTTAAGGAG GCAGATCTC                           579
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Lys Leu Leu Glu Glu Arg Ile Leu Lys Asp Gly His Ile Leu Gly
 1               5                  10                  15
Asp Asn Ile Leu Lys Val Asp Ser Phe Leu Thr His Gln Val Asp Phe
            20                  25                  30
Ser Leu Met Arg Glu Ile Gly Lys Val Phe Ala Glu Lys Phe Ala Ala
        35                  40                  45
Thr Gly Ile Thr Lys Val Val Thr Ile Glu Ala Ser Gly Ile Ala Pro
    50                  55                  60
Ala Val Phe Thr Ala Glu Ala Leu Asn Val Pro Met Ile Phe Ala Lys
65                  70                  75                  80
Lys Ala Lys Asn Ile Thr Met Asn Glu Gly Ile Leu Thr Ala Gln Val
                85                  90                  95
```

```
153  Tyr Ser Phe Thr Lys Gln Val Thr Ser Thr Val Ser Ile Ala Gly Lys
154                  100                 105                 110
155  Phe Leu Ser Pro Glu Asp Lys Val Leu Ile Ile Asp Asp Phe Leu Ala
156              115                 120                 125
157  Asn Gly Gln Ala Ala Lys Gly Leu Ile Gln Ile Ile Glu Gln Ala Gly
158      130                 135                 140
159  Ala Thr Val Gln Ala Ile Gly Ile Val Ile Glu Lys Ser Phe Gln Asp
160  145                 150                 155                 160
161  Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala
162                  165                 170                 175
163  Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp
164                  180                 185                 190
165  Leu
166
167
168            (2) INFORMATION FOR SEQ ID NO:5:
169
170          (i) SEQUENCE CHARACTERISTICS:
171            (A) LENGTH: 25 base pairs
172            (B) TYPE: nucleic acid
173            (C) STRANDEDNESS: single
174            (D) TOPOLOGY: linear
175
176
177          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
178
179  TCCTCAAGGT AGATTCCTTT TTAAC                                        25
180
181            (2) INFORMATION FOR SEQ ID NO:6:
182
183          (i) SEQUENCE CHARACTERISTICS:
184            (A) LENGTH: 20 base pairs
185            (B) TYPE: nucleic acid
186            (C) STRANDEDNESS: single
187            (D) TOPOLOGY: linear
188
189
190          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
191
192  CTCCTTAAAT ACGACCTGAC                                              20
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/896,589*

DATE: 09/03/97
TIME: 13:27:29

INPUT SET: S20087.raw

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